The crystal structure of the rat synapsin I C domain bound to Ca^{2+} and ATP

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ABSTRACT

Synapsins are a group of proteins that have important regulatory functions in synaptic vesicular trafficking. These proteins account for nearly 10% of all proteins on the surface of synaptic vesicles. At least five different synapsins have been identified in mammals. Comparisons of all of the mammalian synapsins has revealed that these proteins are comprised of several conserved domains. All synapsins share the C (or central) domain, which is structurally similar to a family of ATP-utilizing enzymes and is known to bind to ATP *in vitro* [1]. In this study, we have solved the crystal structure of the rat synapsin I C domain bound to Ca^{2+} and ATP. The structure is very similar to that of the bovine C domain [1], but some additional features are present in the rat structure. Several protein loops that were disordered or poorly ordered in the bovine structure are clearly visible in the present structure. Among these loops is a fifteen-residue span that interacts with the bound ATP and other nearby residues. This loop apparently restricts the egress of ATP from its binding site, and obviously could be very important for ATP binding *in vivo*. Also, four crystal forms of rat synapsin I C domain are currently available, and all contain a similar tetramer of synapsin I C monomers. Thus, our studies have demonstrated how Ca^{2+} and ATP interact with this protein, and that the C domain is capable of forming a well-conserved tetramer. Both findings can be experimentally assessed for their relevance *in vitro* and *in vivo*.

REFERENCE

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